

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2003, 16:24:23 ; Search time 15.5429 Seconds
(without alignments)
98.997 Million cell updates/sec

Title: US-09-905-691-5
Perfect score: 16
Sequence: 1 CRRARARARARAE 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	56.2	105	D86976	probable integrat
2	9	56.2	190	B70899	probable mHFP prot
3	8	50.0	336	T50535	isomerase/decarb
4	8	50.0	356	A21198	H-2 class I histoc
5	8	50.0	383	F83490	probable multidrug
6	8	50.0	710	AD3479	ATP-dependent heli
7	8	50.0	897	T02808	conserved hypothet
8	8	50.0	998	T35745	probable ATP-bind
9	7	43.8	69	AD2110	hypothetical prote
10	7	43.8	77	AH0925	hypothetical prote
11	7	43.8	110	T30752	hypothetical prote
12	7	43.8	157	D70777	hypothetical prote
13	7	43.8	159	C83305	hypothetical prote
14	7	43.8	174	D87638	transcription regu
15	7	43.8	252	AH3618	high-affinity bran
16	7	43.8	263	C39741	hypothetical 29K p
17	7	43.8	292	JE0233	troponin-I - scall
18	7	43.8	336	E84295	hypothetical prote
19	7	43.8	358	F87364	Hyd family secret
20	7	43.8	376	T35868	probable dipeptida
21	7	43.8	408	A87649	hypothetical prote
22	7	43.8	409	S72892	probable hexosyltr
23	7	43.8	411	H82998	probable 3-hydroxy
24	7	43.8	428	H87214	probable glycosyl
25	7	43.8	438	T36953	conserved hypothet
26	7	43.8	444	S35783	glycoprotein gA -
27	7	43.8	474	BVBRCE	cyaE protein - Bor
28	7	43.8	480	A70744	probable hexosyltr
29	7	43.8	501	A87474	enoyl-CoA hydratase

30	7	43.8	511	2	B87258	hypothetical prote
31	7	43.8	525	2	A72586	hypothetical prote
32	7	43.8	568	2	B87495	DNA repair protein
33	7	43.8	603	1	Q0BED1	HHLF5 protein - hu
34	7	43.8	604	2	S39885	forked protein - f
35	7	43.8	704	2	T02558	hypothetical prote
36	7	43.8	742	1	TNBBE1	80.7K alpha trans-
37	7	43.8	777	2	A87309	hypothetical prote
38	7	43.8	899	2	C95339	hypothetical prote
39	7	43.8	913	1	VGBEPS	glycoprotein gII p
40	7	43.8	1318	1	Q0BE1	membrane antigen p
41	7	43.8	1360	2	T06699	zinc finger protei
42	7	43.8	1394	2	S60762	IgA-specific serin
43	7	43.8	1403	2	T49093	hypothetical prote
44	6	37.5	65	2	T29066	hypothetical prote
45	6	37.5	68	2	F81055	DNA-directed RNA p

ALIGNMENTS

RESULT 1

D86976
Probable integration host factor [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: D86976
R: Cole, S.T.; Eigemeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.F.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroy, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A: Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, I.
A: Title: Massive gene decay in the leprosy bacillus.
A: Reference number: A86909; MOID: 21128732; PMID: 11234002
A: Accession: D86976
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-105 <STO>
A: Cross-references: GB:AL450380; NID: g13092744; PIDN: CAC30048.1; GSPDB: GN00147
C: Genetics:
A: Gene: mHFP

Query Match

Best Local Similarity 56.2%; Score 9; DB 2; Length 105;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARAE 15

DB 19 AAARRARAE 27

RESULT 2

B70899
Probable mHFP protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: B70899

R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gort; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroy; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A: Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence: A70500; MOID: 98295987; PMID: 9634230

A: Reference number: A70500; MOID: 98295987; PMID: 9634230

A: Accession: B70899

A: Status: preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-190 <COL>

A: Cross-references: GB: A80108; GB: AL123456; NID: g3256012; PIDN: CAB02193.1; PID: g154

A: Experimental source: strain H37RV

C: Genetics:

A: Gene: mHFP

C: Superfamily: Mycobacterium tuberculosis probable mHFP protein

A:Map position: 1

Query Match 50.0%; Score 8; DB 2; Length 897;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARA 14
|||||||
Db 326 AAARRARA 333

RESULT 8

T35745

Probable ATP-binding RNA helicase - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999

R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.

submitted to the EMBL Data Library, August 1999

A:Reference number: Z21588

A:Accession: T35745

A>Status: Preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-998 <SAD>

A:Cross-references: EMBL:AL109732; PIDN:CAB52056.1; GSPDB:GN00070; SCOEDB:SC7H2.14

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SC7H2.14

Query Match 50.0%; Score 8; DB 2; Length 998;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAARRARR 11
|||||||
Db 70 AAARRARR 77

RESULT 9

AD2110

Hypothetical protein asl2435 [Imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C:Accession: AD2110

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchihara, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001.

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AD2110

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-69 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA074134.1; PID:gl7131527; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: asl2435

Query Match 43.8%; Score 7; DB 2; Length 69;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARR 13
|||||||
Db 54 AAARRARR 60

RESULT 10

AH0925

Hypothetical protein STY3665 [Imported] - Salmonella enterica subsp. enterica serovar Typhimurium

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: this species has also been called Salmonella typhi

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AH0925

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church, T.; Cronin, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Far

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001.

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A.; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AH0925

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-77 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD09426.1; PID:gl6504543; GSPDB:GN00176

C:Genetics:

A:Gene: STY3665

Query Match 43.8%; Score 7; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RRARAEA 16
|||||||
Db 30 RRARAEA 36

RESULT 11

T30752

Hypothetical protein 150R - Molluscum contagiosum virus 1

N:Alternate names: MCL50R

C:Species: Molluscum contagiosum virus 1

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000

C:Accession: T30752

R:Senkevich, T.G.; Bugart, J.J.; Sisler, J.R.; Koonin, E.V.; Dairi, G.; Moss, B.

Science 273, 813-816, 1996

A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific hos

A:Reference number: Z20876; MUID:96325459; PMID:8670425

A:Accession: T30752

A>Status: Preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-110 <SEN>

A:Cross-references: EMBL:U60315; NID:gl491943; PIDN:ANC55278.1; PID:gl492093

C:Genetics:

A:Note: MCL50R

C:Superfamily: Molluscum contagiosum virus 1 hypothetical protein 150R

Query Match 43.8%; Score 7; DB 2; Length 110;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRAR 13
|||||||
Db 91 AAARRAR 97

RESULT 12

D70777

Hypothetical protein Rv2322 - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: D70777

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gord

Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroy

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete ge

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: D70777

A>Status: Preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-157 <COL>

A:Cross-references: GB:Z70692; GB:AL123456; NID:g3261567; PIDN:CAA94666.1; PID:el129

Sat Aug 9 19:18:31 2003

Query Match 56.2%; Score 9; DB 2; Length 190;
 Best Local Similarity 100.0%; Pred. No. 0.56; 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 7 AAARRARAE 15
 Db 104 AAARRARAE 112

RESULT 3
 T50935
 isoenzyme/decarboxylase homolog dith [imported] - Pseudomonas abietaniphila
 C:Species: Pseudomonas abietaniphila
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
 C:Accession: T50935
 R:Martin, V.J.; Mohr, W.W.
 J. Bacteriol. 181, 2675-2682, 1999
 A:Title: A novel aromatic-ring-hydroxylating dioxygenase from the diterpenoid-degrading
 A:Reference number: 225281; PMID:10217753
 A:Accession: T50935
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-336 <MAP>
 A:Cross-references: EMBL:AF119621; PIDN:AAD21070.1
 A:Experimental source: strain BME-9; ATCC700689
 C:Genetics:
 A:Gene: dith
 Query Match 50.0%; Score 8; DB 2; Length 336;
 Best Local Similarity 100.0%; Pred. No. 5.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 AAARRARA 14
 Db 105 AAARRARA 112

RESULT 4
 A21198
 H-2 class I histocompatibility antigen pH-2D-24 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Jul-1990 #sequence_revision 31-Jul-1992 #text_change 23-Jul-1999
 R:Allan, J.L.; Cochet, M.; Kummer, A.M.; Gachelin, G.; Kourilsky, P.
 Proc. Natl. Acad. Sci. U.S.A. 80, 7561-7565, 1983
 A:Title: Different exon-intron organization at the 5' part of a mouse class I gene is us
 A:Reference number: A21198; PMID:6143316
 A:Accession: A21198
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-356 <LAL>
 A:Cross-references: GB:K01182; NID:g199544; PIDN:AAA39653.1; PID:g387468
 A:Note: the authors translated the codon CCC for residue 288 as Ser
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 P:205-270/Domain: immunoglobulin homology <IMM>
 Query Match 50.0%; Score 8; DB 2; Length 356;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 RAARRAAR 10
 Db 20 RAARRAAR 27

RESULT 5
 F83490
 Probable multidrug resistance efflux pump PA1237 [imported] - Pseudomonas aeruginosa (st
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: F83490
 R:Stover, C.K.; Pham, X.Q.; Ervin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A:Reference number: A82950; PMID:20437337; PMID:10984043
 A:Accession: F83490
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-383 <STO>
 A:Cross-references: GB:AE004553; GB:AE004091; NID:g9947164; PIDN:AAG04626.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1237
 C:Superfamily: multidrug resistance protein A; lipoyl/biotin-binding homology

Query Match 50.0%; Score 8; DB 2; Length 383;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 ARAARRA 12
 Db 187 ARAARRA 194

RESULT 6
 AD3479
 ATP-dependent helicase hrpB BME11818 [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 14-Apr-2003
 C:Accession: AD3479
 R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanov
 ; Mazur, M.; Goltzman, E.; Selkov, E.; Elser, P.H.; Hagius, S.; O'Callaghan, D.; Let
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
 A:Reference number: AD3479; PMID:11756688
 A:Accession: AD3479
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-710 <KUR>
 A:Cross-references: GB:AE008917; PIDN:AAL52999.1; PID:g17983853; GSPDB:GN00190
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BME11818
 A:Map position: 1
 C:Superfamily: HrpB type ATP-dependent RNA helicase
 Query Match 50.0%; Score 8; DB 2; Length 710;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ARAARR 11
 Db 156 ARAARR 163

RESULT 7
 T02808
 conserved hypothetical protein YPL199c, L2602.6 [imported] - Leishmania major (strai
 C:Species: Leishmania major
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
 C:Accession: D81457; T02808
 R:Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness,
 Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
 A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of prot
 A:Reference number: A81455; PMID:99178987; PMID:10077609
 A:Accession: D81457
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-897 <PKL>
 A:Cross-references: GB:AE001274; NID:g3264850; PIDN:AAC24631.1; PID:g2995584; GSPDB
 A:Experimental source: strain MHOM/IL/81/Friedlin
 C:Genetics:
 A:Gene: L2602.6

A: Experimental source: strain H37Rv
C: Genetics: RV2232
A: Gene: RV2232

Query Match 43.88; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RAAARRA 12
| | | | |
DB 66 RAAARRA 72

RESULT 13

C83305
hypothetical protein PA2721 [Imported] - Pseudomonas aeruginosa (strain PA01)
C: Species: Pseudomonas aeruginosa
C: Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C: Accession: C83305
R: Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A: Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A: Reference number: AB2950; MUID: 20437337; PMID: 10984043
A: Accession: C83305
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-159 <STO>
A: Cross-references: GB:AE004700; GB:AE004091; MID: 99948792; PIDN: AAG06109.1; GSPDB: GN00148
A: Experimental source: strain PA01
C: Genetics:
A: Gene: PA2721

Query Match 43.88; Score 7; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RAAARRA 12
| | | | |
DB 132 RAAARRA 138

RESULT 14

D87638
transcription regulator, Gatr family [Imported] - Caulobacter crescentus
C: Species: Caulobacter crescentus
C: Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C: Accession: D87638
R: Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolodny, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A: Title: Complete Genome Sequence of Caulobacter crescentus.
A: Reference number: AB7249; MUID: 21173698; PMID: 11259647
A: Accession: D87638
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-174 <STO>
A: Cross-references: GB:AE005673; MID: g13424808; PIDN: AAK25104.1; GSPDB: GN00148
C: Genetics:
A: Gene: CC3142

Query Match 43.88; Score 7; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ARAARR 10
| | | | |
DB 50 ARAARR 56

RESULT 15

AH3618
high-affinity branched-chain amino acid transport ATP-binding protein livP BMEII08;
C: Species: Brucella melitensis
C: Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 17-May-2002
C: Accession: AH3618
R: DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivar, J.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A: Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A: Reference number: AD3252; PMID: 11756688
A: Accession: AH3618
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-252 <KUR>
A: Cross-references: GB:AE008918; PIDN: AAL54115.1; PID: g17985076; GSPDB: GN00191
A: Experimental source: strain 16M
C: Genetics:
A: Gene: BMEII0873
A: Map position: II
A: Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
Query Match 43.88; Score 7; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAARRA 8
| | | | |
DB 121 RRAARRA 127

Search completed: August 9, 2003, 16:34:12
Job time: 15.5429 secs